

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using SW model

Run on: March 24, 2003, 15:48:45 ; Search time 4.75152 Seconds

(without alignment)
1133.013 Million cell updates/sec

Title: US-09-988-971-2_COPY_35_90

Sequence: 1 ATAAVALGSPAGPAGPAGLRLR.....VLSEVSGREVNIPSHVAKV 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	35.1	512	1 I56160	protein-tyrosine k
2	101	35.1	512	1 A39719	protein-tyrosine k
3	100	34.7	505	2 I37206	protein-tyrosine k
4	99	34.4	281	2 A57152	src-like adaptor p
5	97	33.7	499	1 A40092	protein-tyrosine k
6	95	33.0	512	1 TVHUTY	protein-tyrosine k
7	92.5	32.1	532	1 B34104	protein-tyrosine k
8	90.5	31.4	509	1 TVHAST	protein-tyrosine k
9	90	31.2	503	1 JQ1321	protein-tyrosine k
10	89.5	31.2	505	1 TVHUC	protein-tyrosine k
11	89.5	31.1	532	1 A34104	protein-tyrosine k
12	89.5	31.1	2415	1 A33733	spectrin alpha cha
13	89	30.9	507	1 A39939	protein-tyrosine k
14	88	30.6	503	1 TVMSHC	protein-tyrosine k
15	88	30.6	509	1 OKHUTK	protein-tyrosine k
16	88	30.6	509	1 I48845	protein-tyrosine k
17	87.5	30.4	526	1 TVFVR	protein-tyrosine k
18	87.5	30.4	526	1 OKFYR	protein-tyrosine k
19	87.5	30.4	526	1 S15582	protein-tyrosine k
20	87.5	30.4	526	2 S20808	protein-tyrosine k
21	87.5	30.4	533	1 TVCHS	protein-tyrosine k
22	87.5	30.4	557	1 TVFVS2	protein-tyrosine k
23	87.5	30.4	568	1 TVFVS1	protein-tyrosine k
24	87.5	30.4	587	1 TVFVR	protein-tyrosine k
25	86.5	30.0	537	1 A45501	protein-tyrosine k
26	85.5	29.7	537	2 I51592	protein-tyrosine k
27	85.5	29.7	539	2 B49114	protein-tyrosine k
28	85.5	29.7	1113	1 A47106	myosin heavy chain
29	84.5	29.3	543	1 TVHUTS	protein-tyrosine k

30	83.5	29.0	534	1 A44991	protein-tyrosine k
31	83.5	29.0	537	1 TVHUTY	protein-tyrosine k
32	83	28.8	228	2 S25730	SH2-SH3 protein se
33	82.5	28.6	468	2 S46791	hypochetrical prote
34	82.5	28.6	528	1 TVFV93	protein-tyrosine k
35	82.5	28.6	537	1 A43806	protein-tyrosine k
36	82.5	28.6	541	1 A43610	protein-tyrosine k
37	82.5	28.6	541	1 TVCHVS	protein-tyrosine k
38	82.5	28.6	542	1 TVHUSC	protein-tyrosine k
39	82.5	28.6	2429	1 SHUA	spectrin alpha cha
40	81.5	28.3	451	2 S58653	hypochetrical prote
41	81.5	28.3	536	2 S33569	protein-tyrosine k
42	81.5	28.3	545	2 S52313	protein-tyrosine k
43	81.5	28.3	546	2 S52314	protein-tyrosine k
44	81.5	28.3	2427	2 T16613	hypochetrical prote
45	80.5	28.0	526	1 TVFV60	protein-tyrosine k

ALIGNMENTS

RESULT 1

156160 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

N.Contains: protein-tyrosine kinase lyn, splice form B

C.Species: Rattus norvegicus (Norway rat)

C.Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #ext_change 18-Feb-2000

C.Accession: I56160, I67811, I67812

R.Mingochi, K.; Nishikata, H.; Sireganian, R.P.

J. Immunol. 150, 222, 1993

A.Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leukocytes

A.Reference number: I56160

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-512 <MIN>

A.Cross-references: GB:I14951, NID:9294582, PIDN:AAA1549.1; PID:9294583

R.Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.

Gene 138, 219-222, 1994

A.Title: The cDNAs encoding two forms of the lyn protein tyrosine kinase are expressed in

A.Reference number: I53715, NID:94171041, PMID:8125304

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID2>

A.Cross-references: GB:I14823, NID:9294580, PIDN:AAA20944.1; PID:9294579

A.Note: in Genbank entry R4TLNATYR, release 116.0, the source is design

A.Cross-references: GB:I14823, NID:9294580, PIDN:AAA20944.1; PID:9294581

A.Note: in Genbank entry R4TLNATYR, release 116.0, the source is design

C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C.Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; 11pore

F.2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MTA>

F.2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MTA>

F.70-118/Domain: SH3 homology <SH3>

F.122-226/Domain: SH2 homology <SH2>

F.245-504/Domain: protein kinase homology <KIN>

F.251-261/Region: protein kinase ATP-binding motif

F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F.275/Active site: lys #status predicted

F.397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 35.1%; Score 101; DB 1; Length 512;

Best Local Similarity 43.4%; Pred. No. 0.00069;

Matches 23; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 4 VALGSPAGPAGPAGPAGLRLR.....VLSEVSGREVNIPSHVAKV 56

Db 69 VALVYDGHIPDLSFKKGKMKVLEHGEWKKAKSLSRKGFIPSHVAKV 121

F/246-254/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/4/Binding site: palmitate (Cys) (covalent) #status predicted
 F/268/Active site: Lys #status predicted
 F/390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 31.2%; Score 90.5; DB 1; Length 509;
 Best Local Similarity 42.3%; Pred. No. 0.011;
 Matches 22; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 4 VALGSPFPGAPALSLRLGEPITV-SEDDGMWTVLSVSGREYNIPSHVAKV 54
 DB 65 VALVDYEAIRHEDLSFQKGDQVWVLESGEWMKARSLATRKEGYIPSNVAVAR 116

RESULT 9

JQ1321
 protein-tyrosine kinase (EC 2.7.1.112) hck - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C/Accession: JQ1321; S18974
 R/Okano, Y.; Sugimoto, Y.; Fukuko, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
 Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
 A/Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
 A/Reference number: JQ1321; MUID:92109719; PMID:1764064
 A/Accession: JQ1321
 A/Molecule type: mRNA
 A/Residues: 1-503 <OKA>
 A/Cross-references: GB:S74141; NID:9241436; PIDN:AA020754.1; PID:9241437
 A/Experimental source: megakaryocyte
 R/Rena, V.; Swaup, G.
 submitted to the EMBL Data Library, December 1991
 A/Reference number: S18974
 A/Accession: S18974
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-50, 'V', 52-204, 'R', 206-305, 'R', 307-503 <RE>
 A/Cross-references: EMBL:X62345; NID:957581; PIDN:CAA44218.1; PID:957582
 C/Genetics:

A/Genes: hck
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming protein kinase
 F/62-110/Domain: SH3 homology <SH3>
 F/121-218/Domain: SH2 homology <SH2>
 F/237-495/Domain: protein kinase homology <KIN>
 F/245-253/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/3/Binding site: palmitate (Cys) (covalent) #status predicted
 F/267/Active site: Lys #status predicted
 F/388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 31.2%; Score 90; DB 1; Length 503;
 Best Local Similarity 35.8%; Pred. No. 0.013;
 Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 4 VALGSPFPGAPALSLRLGEPITV-SEDDGMWTVLSVSGREYNIPSHVAKV 56
 DB 61 VALVDYEAIRHEDLSFQKGDQVWVLESGEWMKARSLATRKEGYIPSNVAVAR 113

RESULT 10

TVRHUC
 protein-tyrosine kinase (EC 2.7.1.112) hck - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1998 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
 C/Accession: A27811; A27812; J01149; C38268; S31103
 R/Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettinati, M.J.; Le Beau, M.M.; Die Mol. Cell. Biol. 7, 2267-2275, 1987
 A/Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
 A/Reference number: A27811; MUID:87257942; PMID:3496523
 A/Accession: A27811
 A/Molecule type: mRNA

A/Residues: 1-505 <OUT>

A/Cross-references: GB:M16591

A/Note: the codon given for 3-Cys (TTC) is inconsistent with the authors' translation
 R/Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
 Mol. Cell. Biol. 7, 2276-2285, 1987

A/Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h

A/Reference number: A27812; MUID:87257943; PMID:3453117

A/Accession: A27812

A/Molecule type: mRNA

A/Residues: 1-505 <ZIR>

A/Cross-references: GB:M16592; NID:9183913; PIDN:AA02644.1; PID:9306833

R/Hradezky, D.; Strebhardt, K.; Rubsamann-Waigmann, H.
 Gene 113, 275-280, 1992

A/Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase

A/Reference number: J01149; MUID:92241880; PMID:1572549

A/Accession: J01149

A/Molecule type: DNA

A/Residues: 157-505 <HRA>

A/Cross-references: EMBL:X59741

R/Partanen, J.; Maekelae, T.P.; Allitalo, R.; Lehtvaesaho, H.; Allitalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A/Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A/Reference number: A38268; MUID:91062389; PMID:2247464

A/Accession: C38268

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 362-417 <PAR>

A/Genetics:

A/Genes: HCK

A/Cross-references: GDB:119303; OMIM:142370

A/Map position: 20q11-20q12

A/Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1

C/Function:

A/Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphatase

F/2-505/Product: protein-tyrosine kinase hck #status predicted <MNT>

F/64-112/Domain: SH3 homology <SH3>

F/123-220/Domain: SH2 homology <SH2>

F/239-497/Domain: protein kinase homology <KIN>

F/247-255/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/3/Binding site: palmitate (Cys) (covalent) #status predicted

F/269/Active site: Lys #status predicted

F/390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 31.2%; Score 90; DB 1; Length 505;

Best Local Similarity 35.8%; Pred. No. 0.013;
 Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 4 VALGSPFPGAPALSLRLGEPITV-SEDDGMWTVLSVSGREYNIPSHVAKV 56
 DB 63 VALVDYEAIRHEDLSFQKGDQVWVLESGEWMKARSLATRKEGYIPSNVAVAR 115

RESULT 11

A34104
 protein-tyrosine kinase (EC 2.7.1.112) src 1 [similarity] - African clawed frog
 N/Alternate names: kinase-related transforming protein (src); kinase-related transforming protein
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
 C/Accession: A34104; I51564
 R/Steale, R.E.; Unger, T.F.; Mardis, M.J.; Ferro, J.B.
 J. Biol. Chem. 264, 10649-10653, 1989
 A/Title: The two Xenopus laevis src genes are co-expressed and each produces functional
 A/Reference number: A34104; MUID:99278134; PMID:2493582
 A/Accession: A34104
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-532 <STE>
 A/Cross-references: GB:M24704; GB:J04822; NID:9214804; PIDN:AAA49962.1; PID:9214805
 R/Steale, R.E.; Choen, R.; Ral, B.B.A.; Minokur, S.T.; Unger, T.F.
 Oncogene 7, 2345-2350, 1992

C:Accession: A27282; A39973
 R:Klemas, M.J.; McKercher, S.R.; Maki, R.A.
 Nucleic Acids Res. 15, 9600, 1987
 A:Title: Nucleotide sequence of the mouse hck gene.
 A:Reference number: A27282; MUID:88067781; PMID:3684607
 A:Accession: A27282
 A:Molecule type: mRNA
 A:Residues: 1-503 <KLE>
 A:Cross-references: GB:Y00487; NID:951209; PIDN:CA68544.1; PID:951210
 R:Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
 A:Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
 A:Reference number: A39973; MUID:88065587; PMID:3317404
 A:Accession: A39973
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-503 <HOL>
 A:Cross-references: GB:U03023; NID:9192212; PIDN:AAA37305.1; PID:9309118
 C:Genetics:
 A:Gene: hck
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F:62-110/Domain: SH3 homology <SH2>
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase homology <KIN>
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388/499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 30.6%; Score 88; DB 1; Length 503;
 Best Local Similarity 35.8%; Pred. No. 0.022;
 Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 4 VALGSPAGPAPLRLAGEPLTIVSEGDGMWTVLSEVSGENIPSHVAKV 56
 DB 61 VALHYEAIHREDSPQKQDQWVLEENGEMWKRSLATKGGYIPSNVAVR 113

RESULT 15
 OKHOLK
 N:Alternate names: kinase-related transforming protein (lck)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text change 28-Jan-2000
 C:Accession: JQ0152; S07822; S07200; S01879; S07143; A32757; I57636
 R:Rouet, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
 Gene 84, 105-113, 1989
 A:Title: Structure of the human lck gene: differences in genomic organisation within src
 A:Reference number: JQ0152; MUID:90108697; PMID:2558056
 A:Accession: JQ0152
 A:Molecule type: DNA
 A:Residues: 1-509 <ROU>
 A:Cross-references: EMBL:X14053
 R:Perlmuter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
 J. Cell. Biochem. 38, 117-126, 1989
 A:Title: Structure and expression of lck transcripts in human lymphoid cells.
 A:Reference number: S07822; MUID:89123626; PMID:3365417
 A:Accession: S07822
 A:Molecule type: mRNA
 A:Residues: 1-86; 'P', 88-509 <PER>
 A:Cross-references: EMBL:X13529; NID:934294; PIDN:CA63184.1; PID:934295
 R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolaki, R.; Yanagi, Y.; Yoshikaki, Y.; Mak, T.W.
 Eur. J. Immunol. 16, 1643-1646, 1986
 A:Title: A human T cell-specific cDNA clone (YTI6) encodes a protein with extensive homol
 A:Reference number: S07200; MUID:87133831; PMID:3493153
 A:Accession: S07200
 A:Molecule type: mRNA
 A:Residues: 1-205; 'ASAIRPI', 212-257; 'RCGW', 262; 'TTT', 266; 'T', 268-281; 'AGRLP', 287-503; 'ST
 A:Cross-references: EMBL:X05027; NID:936807; PIDN:CA628691.1; PID:936808
 R:Veilleux, A.; Rose, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.
 Oncogene Res. 1, 357-374, 1987

A:Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
 A:Reference number: S01879; MUID:88217332; PMID:2835736
 A:Accession: S01879
 A:Molecule type: mRNA
 A:Residues: 368-471; 'H', 473-509 <VEI>
 A:Cross-references: EMBL:X06369; NID:934288; PIDN:CA629667.1; PID:934289
 R:Trevisan, U.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canina, C.; Lima, T.J.
 Biochem. Biophys. Acta 888, 286-295, 1986
 A:Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (lck).
 A:Reference number: S07143; MUID:87000726; PMID:3489486
 A:Accession: S07143
 A:Molecule type: mRNA
 A:Residues: 'A', 376-509 <TRS>
 A:Cross-references: EMBL:X04476; NID:935779; PIDN:CA628165.1; PID:935780
 R:Takadera, T.; Leung, S.; Geronzi, A.; Koga, Y.; Takahara, Y.; Miyamoto, N.G.; Mak, T.W.
 Mol. Cell. Biol. 9, 2173-2180, 1989
 A:Title: Structure of the two promoters of the human lck gene: differential accumulation
 A:Reference number: A32797; MUID:89313764; PMID:2787474
 A:Accession: A32797
 A:Molecule type: DNA
 A:Residues: 1-35 <TK>
 A:Cross-references: GB:M26692; NID:9341523; PIDN:AAA59503.1; PID:9349702
 R:Garvin, A.M.; Fawcett, S.; Marth, J.D.; Perlmuter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
 A:Reference number: I57636; MUID:89096891; PMID:2850479
 A:Accession: I57636
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35; 'VR' <RES>
 A:Cross-references: GB:M2510; NID:9187031; PIDN:AAA5501.1; PID:955352
 C:Comment: Protein tyrosine kinases play important roles in the control of cell growth a
 C:Genetics:
 A:Gene: GDB:153390
 A:Cross-references: GDB:119360; OMIM:153390
 A:Map position: 1p35-1p34.3
 A:Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
 F:68-116/Domain: SH3 homology <SH2>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:273/Active site: Lys #status predicted
 F:394/505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 30.6%; Score 88; DB 1; Length 509;
 Best Local Similarity 36.5%; Pred. No. 0.022;
 Matches 19; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

QY 4 VALGSPAGPAPLRLAGEPLTIVSEGDGMWTVLSEVSGENIPSHVAKV 55
 DB 67 IALHSYPSHDGDLGKRGKQRLILBOSGEMWKAQSLTTGGEGTIPNVAVK 118

Search completed: March 24, 2003, 15:51:40
 Job time: 5.75152 secs